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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=24; hr=14; min=16; sec=47; ms=367;]

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Reviewer Comments:

<210> 4

<211> 25

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: GRK6 peptide
sequence

<400> 4

Leu	Leu	Gln	Arg	Leu	Phe	Ser	Arg	Gln	Asp	Cys	Cys	Gly	Asn	Cys	Ser
1				5					10					15	

Asp	Ser	Glu	Glu	Glu	Leu	Pro	Thr	Arg
			20					25

The above <213> response is invalid, per Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." (do not add "Organism" to it). This error appears in subsequent sequences, too.

Application No: 10588114 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-01-14 17:30:10.651
Finished: 2008-01-14 17:30:18.512
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 861 ms
Total Warnings: 67
Total Errors: 0
No. of SeqIDs Defined: 99
Actual SeqID Count: 99

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
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W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (7)
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W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
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W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)

Input Set:

Output Set:

Started: 2008-01-14 17:30:10.651
Finished: 2008-01-14 17:30:18.512
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 861 ms
Total Warnings: 67
Total Errors: 0
No. of SeqIDs Defined: 99
Actual SeqID Count: 99

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10588114

<141> 2008-01-14

<150> PCT/US05/002633

<151> 2005-01-28

<150> 60/628,997

<151> 2004-11-18

<150> 60/607,684

<151> 2004-09-07

<150> 60/557,152

<151> 2004-03-26

<150> 60/539,774

<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide linker

<400> 1

Gly Ser Gly Gly Gly
1 5

<210> 2

<211> 37

<212> PRT

<213> Homo sapiens

<400> 2

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr

Met Gly Leu Leu Thr
35

<210> 3
<211> 14
<212> PRT
<213> Rous sarcoma virus

<400> 3
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 4
<211> 25
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: GRK6 peptide
sequence

<400> 4
Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg
20 25

<210> 5
<211> 7
<212> PRT
<213> Monkey virus SV40

<400> 5
Pro Lys Lys Lys Lys Lys Val
1 5

<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

<400> 6
Ala Arg Arg Arg Arg Pro
1 5

<210> 7
<211> 10
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: NF kappa-B p50
sequence

<400> 7

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 8

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: NF kappa-B p65
sequence

<400> 8

Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 9

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Nucleoplasmin
sequence

<400> 9

Ala Val Lys Arg Pro Ala Ala Thr Leu Lys Lys Ala Gly Gln Ala Lys
1 5 10 15

Lys Lys Lys Leu Asp
20

<210> 10

<211> 5

<212> PRT

<213> Homo sapiens

<400> 10

Lys Phe Glu Arg Gln
1 5

<210> 11

<211> 36

<212> PRT

<213> Homo sapiens

<400> 11

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
20 25 30

Tyr Gln Thr Ile
35

<210> 12

<211> 35

<212> PRT

<213> Homo sapiens

<400> 12

Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 13

<211> 27

<212> PRT

<213> Saccharomyces cerevisiae

<400> 13

Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 14

<211> 25

<212> PRT

<213> Saccharomyces cerevisiae

<400> 14

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

<210> 15

<211> 64

<212> PRT

<213> Saccharomyces cerevisiae

<400> 15

Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
1 5 10 15
Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
20 25 30
Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
35 40 45
Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
50 55 60

<210> 16

<211> 41

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
1 5 10 15
Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
20 25 30
Gln Gln Gln Gln Gln Arg Gly Lys Lys
35 40

<210> 17

<211> 4

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Endoplasmic
reticulum localizing sequence

<400> 17

Lys Asp Glu Leu
1

<210> 18

<211> 15

<212> PRT

<213> Human adenovirus type 19

<400> 18

Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
1 5 10 15

<210> 19
<211> 20
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Interleukin-2
sequence

<400> 19
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 20
<211> 29
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 21
<211> 27
<212> PRT
<213> Homo sapiens

<400> 21
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 22
<211> 18
<212> PRT
<213> Influenza A virus

<400> 22
Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 23

<211> 24
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Interleukin-4
 sequence

 <400> 23
 Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
 1 5 10 15

 Cys Ala Gly Asn Phe Val His Gly
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<210> 24
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 24
 tgccg gatcc ggcggtggcc acccagaaac gctggtg 37

<210> 25
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 25
 gtctgaggat ccccaatgct taatcagtga 30

<210> 26
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 26
 gccgttaatc cagattac 18

<210> 27
 <211> 41

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <220>
 <221> modified_base
 <222> (18)..(19)
 <223> a, c, g, t, unknown, or other

 <220>
 <221> modified_base
 <222> (21)..(22)
 <223> a, c, g, t, unknown, or other

 <400> 27
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 <210> 28
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 28
 gaagataatg tcagggcc 18

 <210> 29
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

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 <221> modified_base
 <222> (19)..(20)
 <223> a, c, g, t, unknown, or other

 <400> 29
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 <210> 30
 <211> 18
 <212> DNA
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<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 30
aacagcgatc gggtaagc 18

<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 31
gcttaccgga tcgctgttnn kgcgttatcg ctgatttat 39

<210> 32
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 32
cgggccgttg atggtcac 18

<210> 33
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 33
atgaccatca acggcccgnn kgcacgtgcc aacatcgac 39

<210> 34
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 34
atccggacta gtaggccttt acttggatgat acgagt 36

<210> 35
<211> 1995
<212> DNA
<213> Escherichia coli

<400> 35
atgaaaataa aaacaggtgc acgcatactc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccttg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
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ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
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ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
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gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tgggacaaga gccaccaga aacgctgggtg aaagtaaaag atgctgaaga tcagttgggt 1440
gcacgagtgg gttacatcga actggatctc aacagcggta agatccttga gagttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagtgc tgctatgtgg cgcggtatta 1560
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atcgaggagc cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcgtt gggaaccgga actgaatgaa gccgcgccca ccatggaaaa cgcccagaaa 1860
gggtgaaatca tgccgaacat cccgcagatg tccgctttct ggtatgccgt gcgtactgcg 1920
gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980
cgtatcacca agtaa 1995

<210> 36
<211> 664

<212> PRT

<213> Escherichia coli

<400> 36

Met	Lys	Ile	Lys	Thr	Gly	Ala	Arg	Ile	Leu	Ala	Leu	Ser	Ala	Leu	Thr
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			20					25					30		
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu
		35					40					45			
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu
	50					55					60				
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly
65					70					75					80
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr
				85					90					95	
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln
			100					105					110		
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys
		115					120					125			
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn
	130					135						140			
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala
145					150					155					160
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn
				165					170					175	
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly
			180					185					190		
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly
	195						200					205			
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu
	210					215					220				
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu
225					230					235					240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp
				245					250					255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
			260					265					270		
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
	275						280						285		

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
 340 345 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
 355 360 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
 370 375 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
 385 390 395 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
 405 410 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
 420 425 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
 435 440 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
 450 455 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
 500 505 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 530